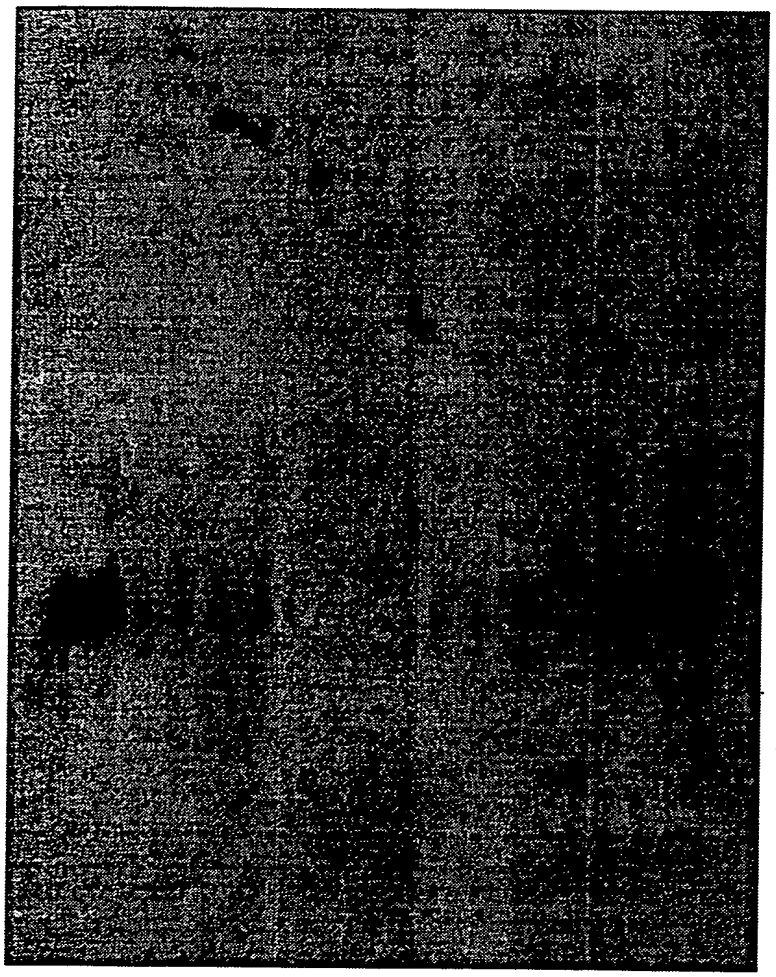

Fig. 1A

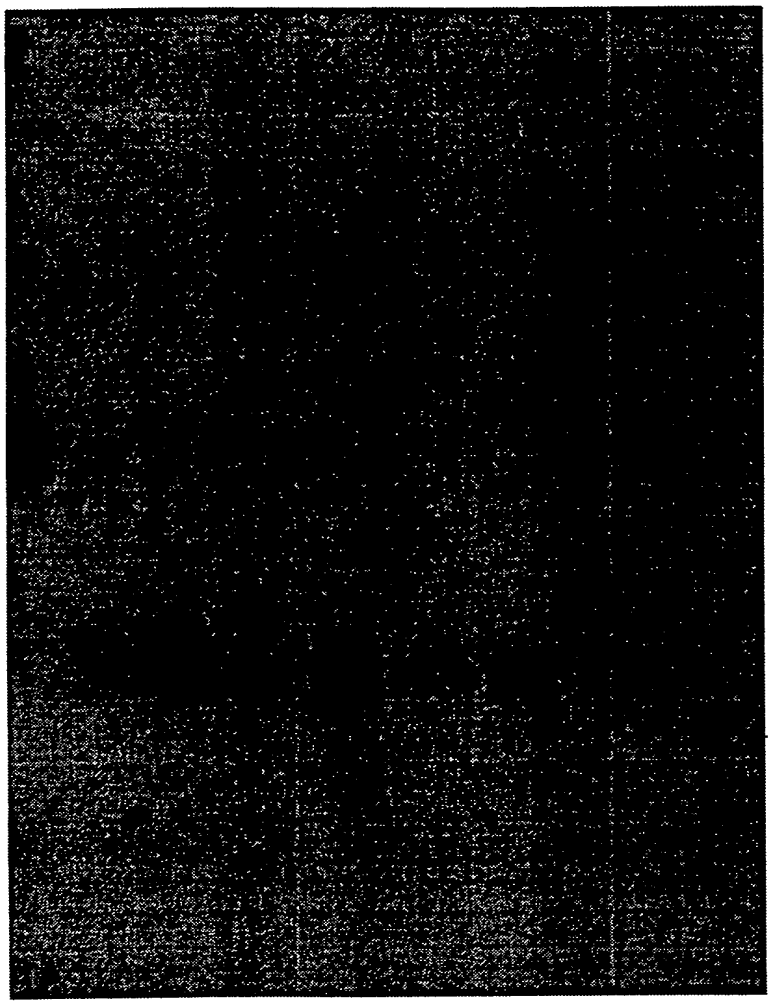

Fig. 1B

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  53 TCTTCAACTCCAGCTTAGAAGTGCCTGCCTGGCTCAGGGTCTGCACTGCAGCCTACTCCT
 113 TGCTTCAGGGCCTGACTGCAACGCCAAAGCCTATCCTATAGCGGCAGCGCCAGCAGCCAC
 173 TCAAACCAGCCACAGCTCCCCGGCAACCGAACCATGAACACCGAAATGTATCAGACCCCC
                                      MetAsnThrGluMetTyrGlnThrPro

 233 ATGGAGGTGGCGGTCTATCAGCTGCACAATTTCTCCACCTCCTTCTTTTCTTCTCTGCTT
     MetGluValAlaValTyrGlnLeuHisAsnPheSerThrSerPhePheSerSerLeuLeu

 293 GGAGGGGATGTGGTTTCCGTTAAACTGGATAACAGTGCCTCCGGAGCCAGTGTGGTGGCC
     GlyGlyAspValValSerValLysLeuAspAsnSerAlaSerGlyAlaSerValValAla

 353 CTAGACAACAAGATTGAGCAGGCCATGGACCTCGTGAAGAACCACCTGATGTACGCTGTG
     LeuAspAsnLysIleGluGlnAlaMetAspLeuValLysAsnHisLeuMetTyrAlaVal

 413 AGAGAGGAGGTGGAGGTCCTAAAGGAGCAGATTCGTGAGCTGCTTGAGAAGAACTCCCAG
     ArgGluGluValGluValLeuLysGluGlnIleArgGluLeuLeuGluLysAsnSerGln

 473 CTGGAGCGCGAGAACACCCTCCTGAAGACGCTGGCAAGCCCCGAGCAACTGGAAAAGTTC
     LeuGluArgGluLeuThrLeuLeuLysThrLeuAlaSerProGluGlnLeuGluLysPhe

 533 CAGTCCCGGCTGAGCCCTGAAGAGCCAGCACCTGAAGCCCCAGAAACCCCGGAAACCCCG
     GlnSerArgLeuSerProGluGluProAlaProGluAlaProGluThrProGluThrPro

 593 GAAGCCCCTGGTGGTTCTGCGGTGTAAGTGGCTCTGTCCTTAGGGTGGGCAGAGCCACAT
     GluAlaProGlyGlySerAlaVal *

 653 CTTGTTCTACCTAGTTCTTTCCAGTTTGTTTTTGGCTCCCCAAGGGTCATCTCATGTGGA
 713 GAACTTTACACCTAACATAGCTGGTGCCAAGAGATGTCCCAAGGACATGCCCATCTGGGT
 773 CCACTCCAGTGACAGACCCCTGACAAAGAGCAGGTCTCTGGAGACTAAGTTGCATGGGGC
 833 CTAGTAACACCAAGCCAGTGAGCCTGTCGTGTCACCGGGCCCTGGGGGCTCCCAGGGCTG
 893 GGCAACTTAGTTACAGCTGACCAAGGAGAAAGTAGTTTTGAGATGTGATGCCAGTGTGCT
 953 CCAGAAAGTGTAAGGGGTCTGTTTTTCATTTCCATGGACATCTTCCACAGCTTCACCTGA
1013 CAATGACTGTTCCTATGAAGAAGCCACTTGTGTTCTAAGCAGAAGCAACCTCTCTCTTCT
1073 TCCTCTGTCTTTTCCAGGCAGGGGCAGAGATGGGAGAGATTGAGCCAAATGAGCCTTCTG
1113 TTGGTTAATACTGTATAATGCATGGCTTTGTGCACAGCCCAGTGTGGGGTTACAGCTTTG
1193 GGATGACTGCTTATAAAGTTCTGTTTGGTTAGTATTGGCATCGTTTTTCTATATAGCCAT
1253 AATGCGTATATATACCCATAGGGCTAGATCTATATCTTAGGGTAGTGATGTATACATATA
1313 CACATACACCTACATGTTGAAGGGCCTAACCAGCTTTGGGAGTACTGACTGGTCTCTTAT
1373 CTCTTAAAGCTAAGTTTTTGACTGTGCTAATTTACCAAATTGATCCAGTTTGTCCTTTAG
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1733 GTTAATCAAAGGATGTAGTCCTGTGGTAGACCAGAGGAGTAACTAGTTTTGATCCTTTGG
1793 GGTGTGGAAAATGTACCCAGGAAGCTTGTGTAAGGAGGTTCTGTGACAGTGAACACTTTC
1853 CACTTTCTGACACCTCATCCTGCTGTACGACTCCAGGATTTGGATTTGGATTTTTCAAAT
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Fig. 2

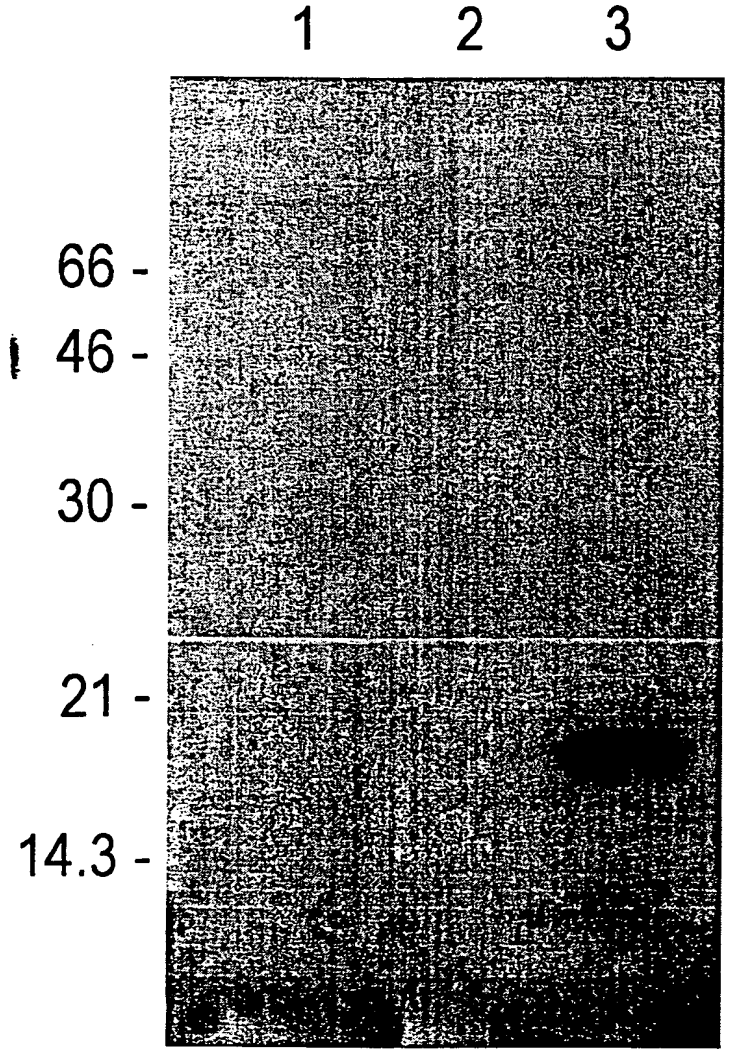


Fig. 3A

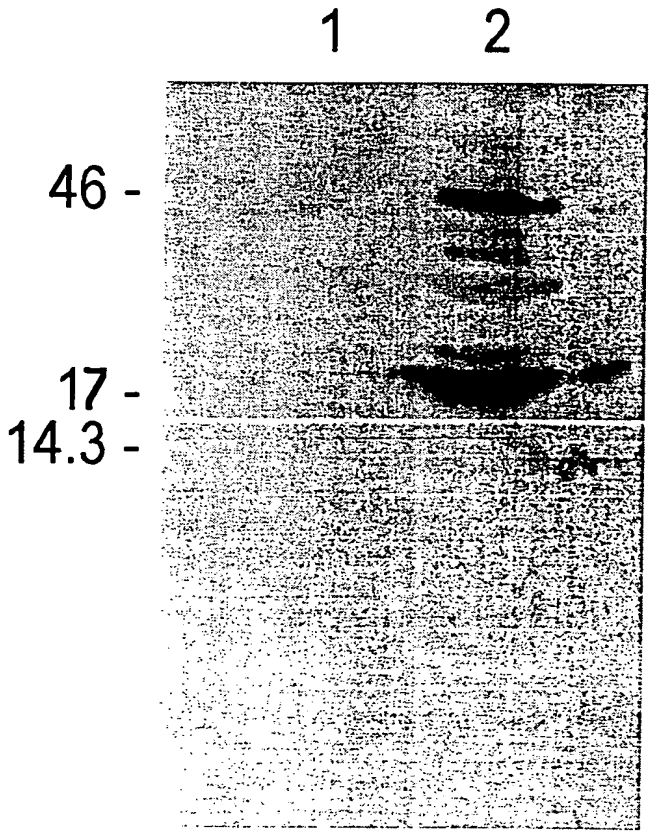


Fig. 3B

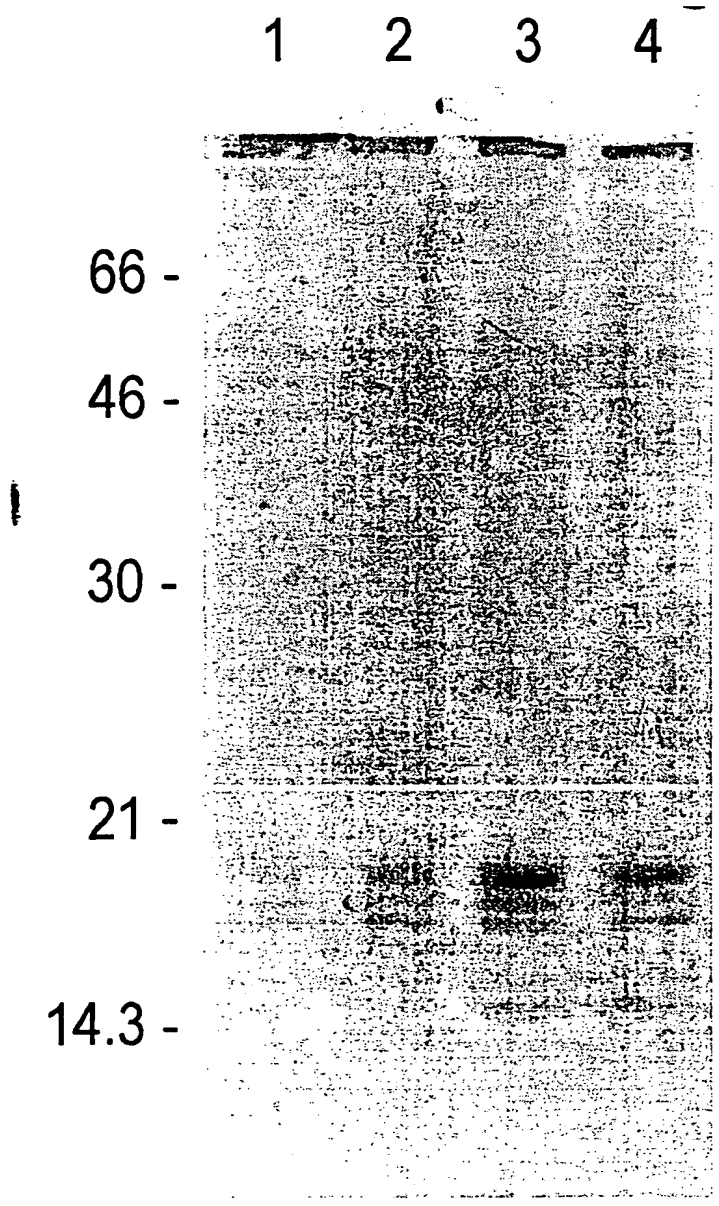


Fig. 3C

09/403861

GILR	L	K	E	Q	I	R	E	L	L	E	K	N	S	Q	L	E	R	E	N	T	L	L	K	T	L	A
TSC-22	L	K	E	Q	I	K	E	L	I	E	K	N	S	Q	L	E	Q	E	N	D	L	L	K	T	L	A
GCN4	L	E	D	K	V	E	E	L	L	S	K	N	Y	H	L	E	N	E	V	A	R	L	K	K	L	V
CREB	L	E	N	R	V	A	V	L	E	N	Q	N	K	T	L	I	E	E	L	K	A	L	K	D	L	Y
CREM	L	E	N	R	V	A	V	L	E	N	Q	N	K	T	L	I	E	E	L	K	A	L	K	D	L	Y
c-jun	L	E	E	K	V	K	T	L	K	A	Q	N	S	E	L	A	S	T	A	N	M	L	R	E	Q	V

Fig. 4

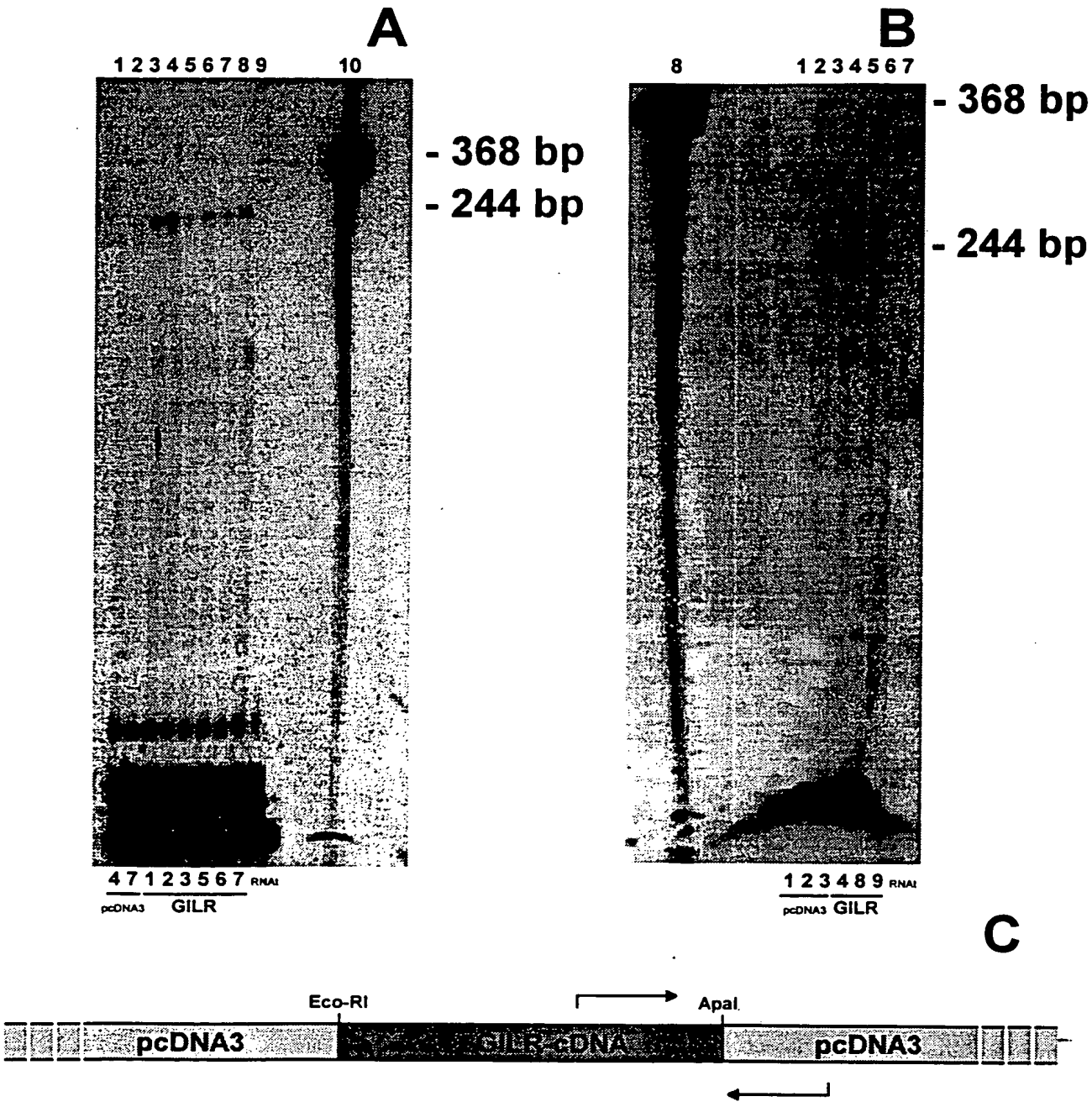


Fig. 5

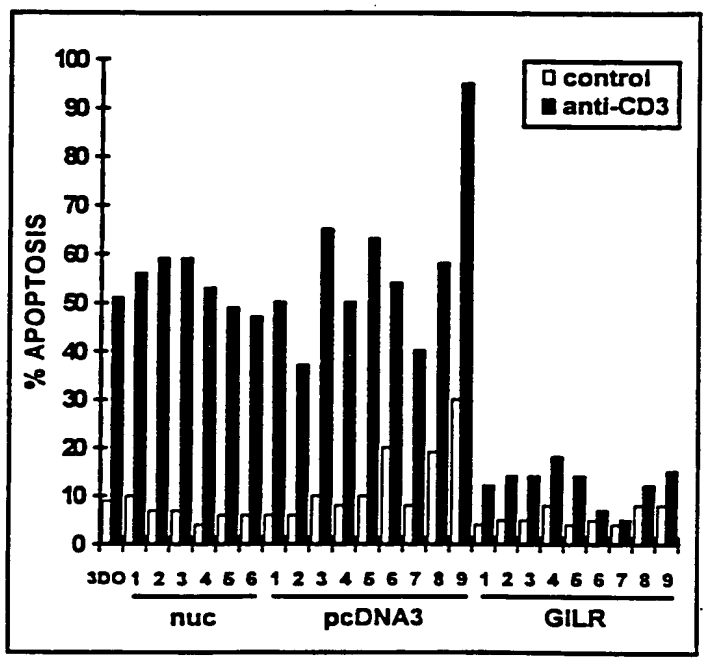


Fig. 6

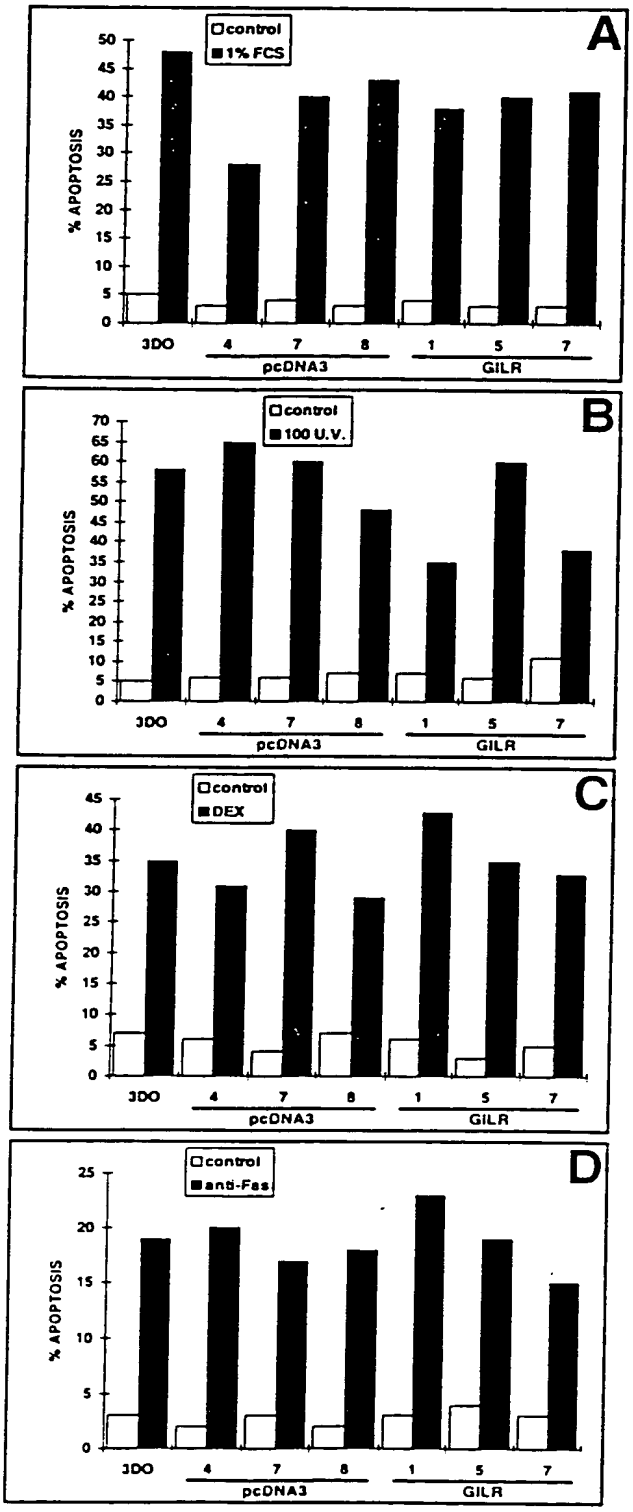

A
control
1% FCS
% APOPTOSIS
3DO
4
7
8
1
5
7
pcDNA3
GILR
B
control
100 U.V.
% APOPTOSIS
3DO
4
7
8
1
5
7
pcDNA3
GILR
C
control
DEX
% APOPTOSIS
3DO
4
7
8
1
5
7
pcDNA3
GILR
D
control
anti-Fas
% APOPTOSIS
3DO
4
7
8
1
5
7
pcDNA3
GILR

Fig. 7

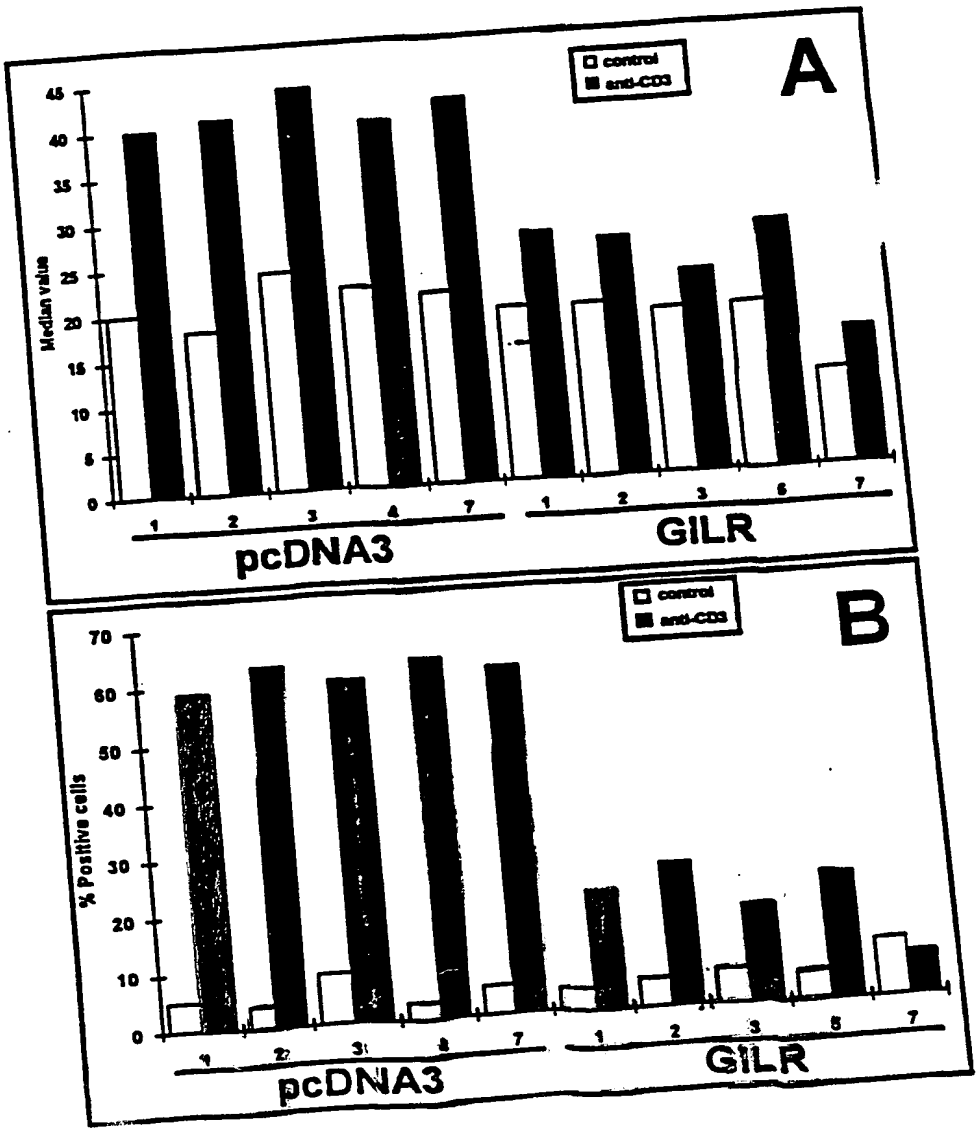
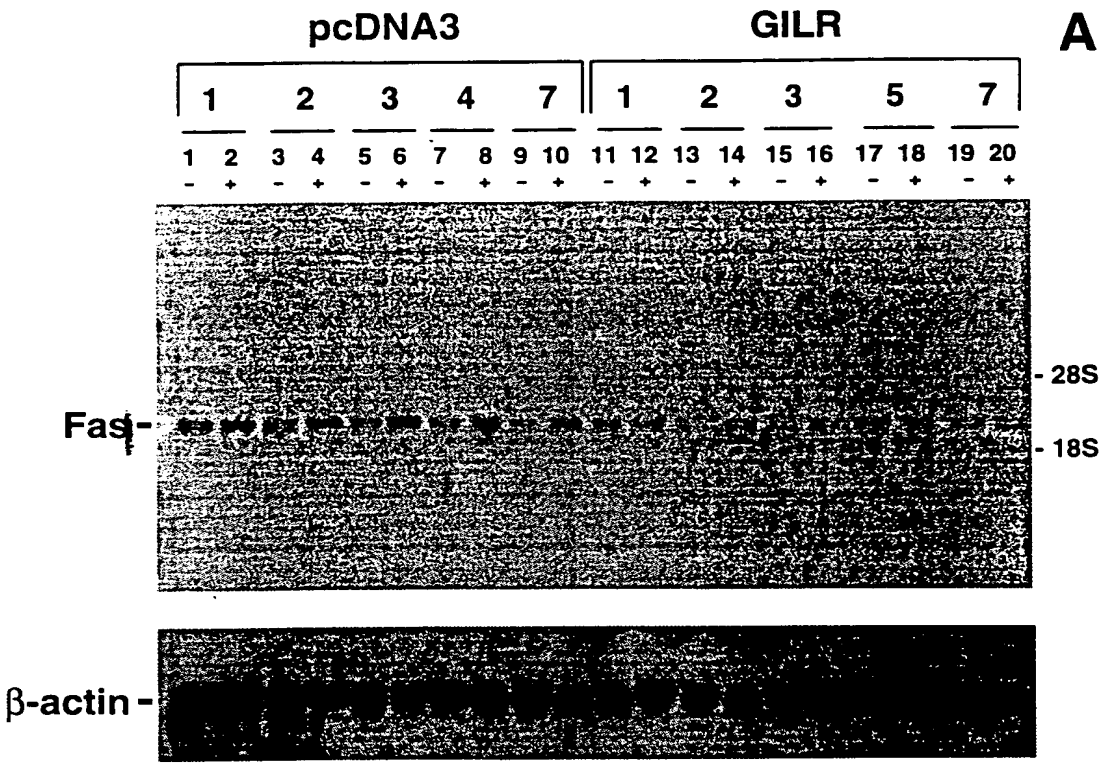

A
control
anti-CD3
Median value
pcDNA3
GILR
B
control
anti-CD3
% Positive cells
pcDNA3
GILR

Fig 3



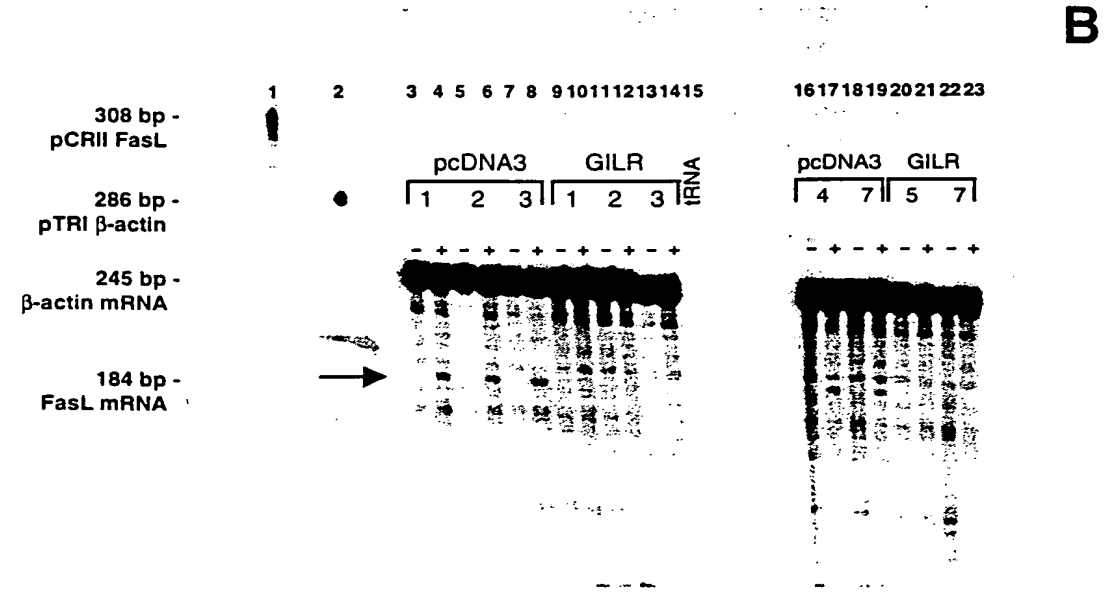
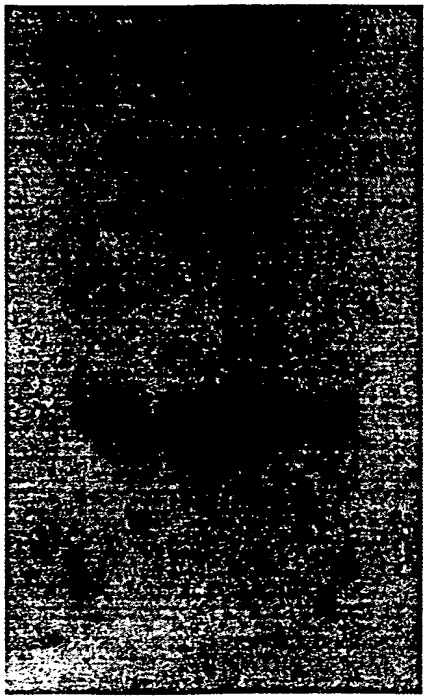
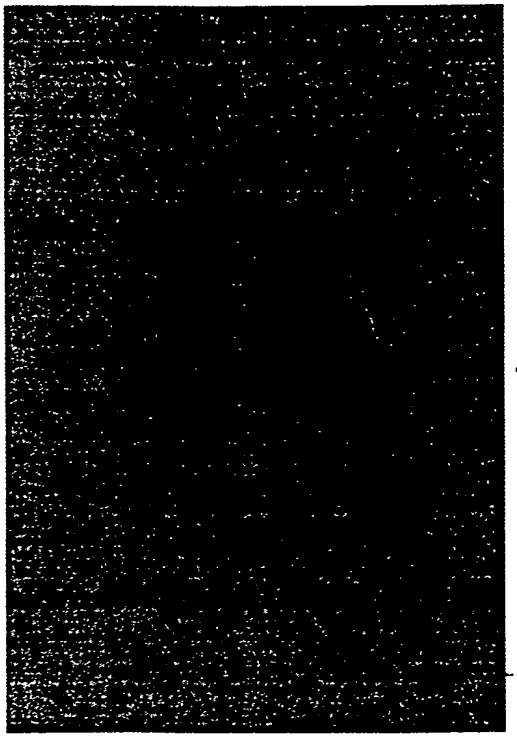


Fig. 9





A

B

Fig. 10

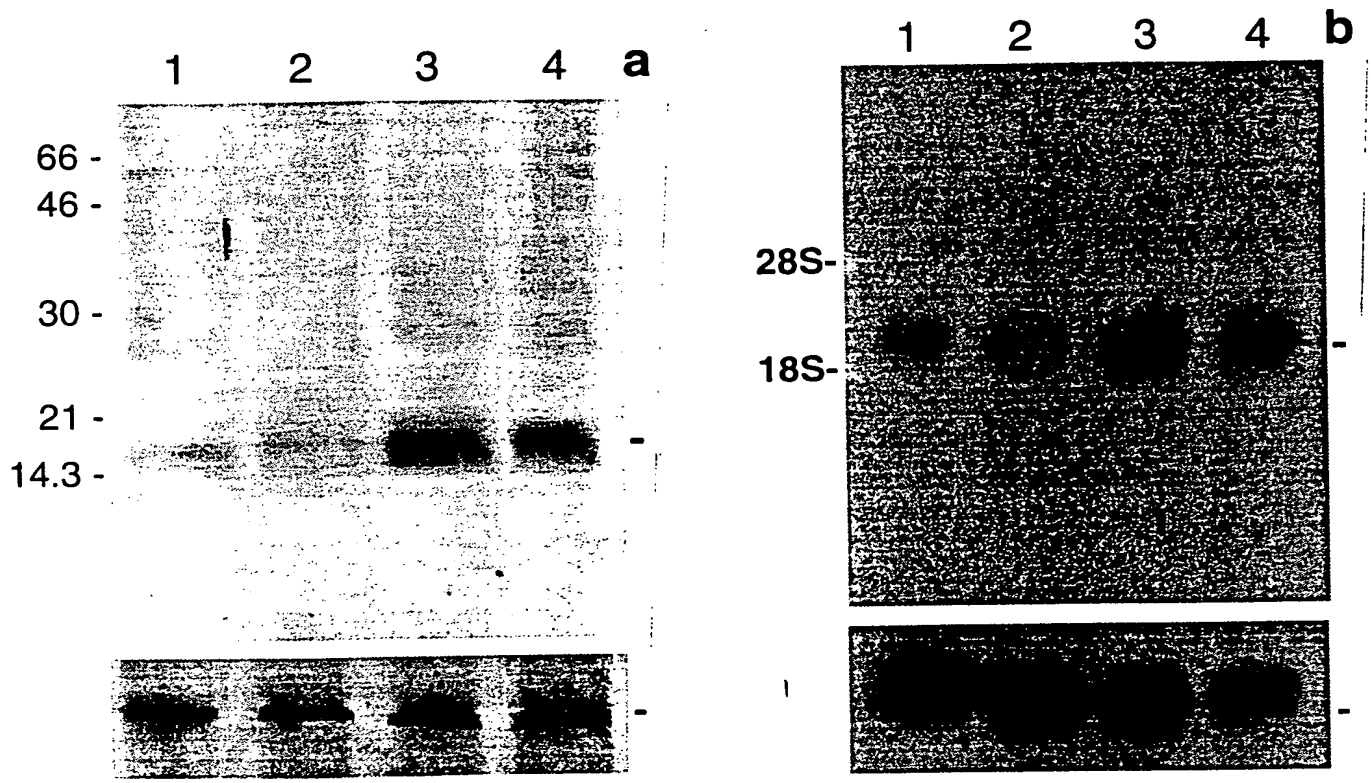


Fig. 11

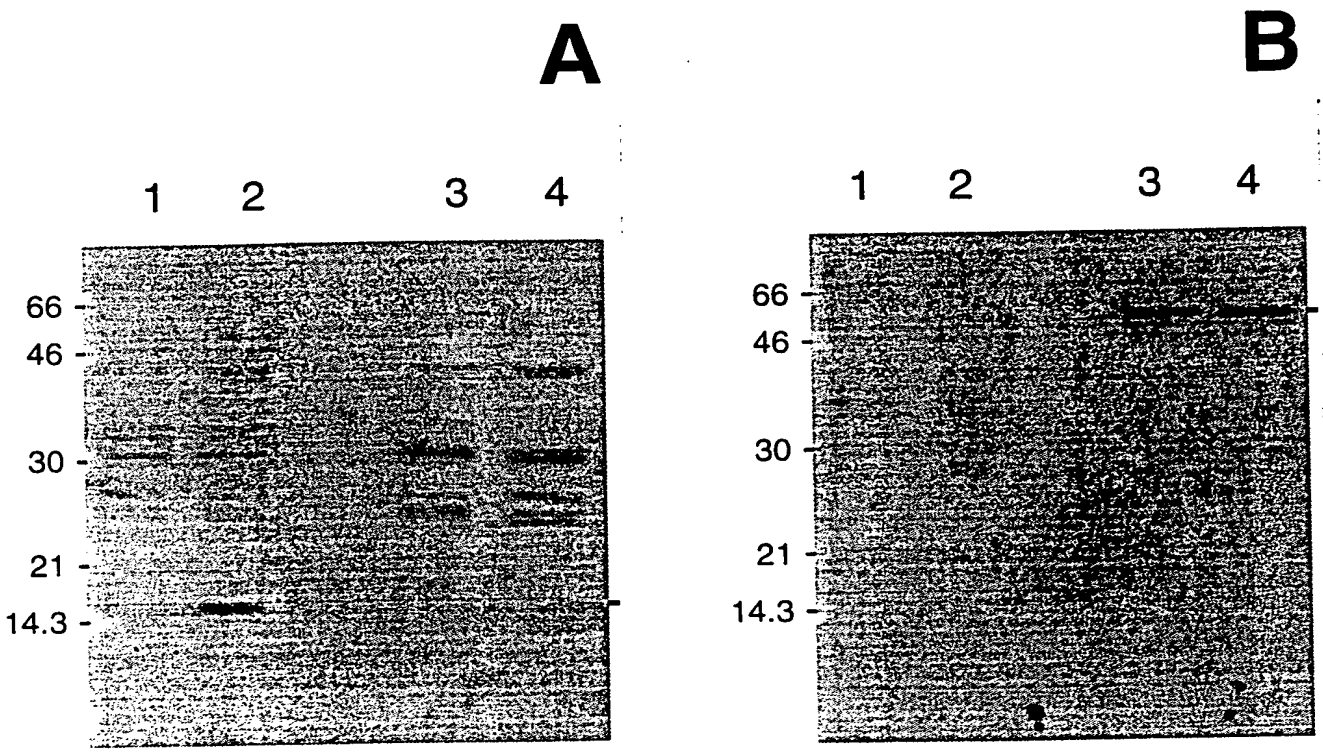


Fig. 12

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 121 AGCCTCAGGGCCGGACTCCAGCGCAGAGCCCAGCCCAGCGCAGCCTGCCAGCAGCCACCC
 181 AGCCGCCCAGCCGCCCAGCCCCGCACGAAACCCGGCCAGAGCTTCCTAGCAGCCCGAGCC
 241 ATGAACACCGAAATGTATCAGACCCCCATGGAGGTGGCGGTCTACCAGCTGCACAATTTC
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 301 TCCATCTCCTTCTTCTCTTCTCTGCTTGGAGGGGATGTGGTTTCCGTTAAGCTGGACAAC
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 361 AGTGCCTCCGGAGCCAGCGTGGTGGCCATAGACAACAAGATCGAACAGGCCATGGATCTG
     SerAlaSerGlyAlaSerValValAlaIleAspAsnLysIleAspGlnAlaMetAspLeu

 421 GTGAAGAATCATCTGATGTATGCTGTGAGAGAGGAGGTGGAGATCCTGAAGGAGCAGATC
     ValLysAsnHisLeuMetTyrAlaValArgGluGluValGluIleLeuLysGluGlnIle

 481 CGAGAGCTGGTGGAGAAGAACTCCCAGCTAGAGCGTGAGAACACCCTGTTGAAGACCCTG
     ArgGluLeuValGluLysAsnSerGlnLeuGluArgGluAsnThrLeuLeuLysThrLeu

 541 GCAAGCCCAGAGCAGCTGGAGAAGTTCCAGTCCTGTCTGAGCCCTGAAGAGCCAGCTCCC
     AlaSerProGluGlnLeuGluLysPheGlnSerCysLeuSerProGluGluProAlaPro

 601 GAATCCCCACAAGTGCCCGAGGCCCCTGGTGGTTCTGCGGTGTAAGTGGCTCTGTCCTCA
     GluSerProGlnValProGluAlaProGlyGlySerAlaVal *

 661 GGGTGGGCAGAGCCACTAAACTTGTTTTACCTAGTTCTTTCCAGTTTGTTTTTGGCTCCC
 721 CAAGCATCATCTCACGAGGAGAACTTTACACCTAGCACAGCTGGTGCCAAGAGATGTCCT
 781 AAGGACATGGCCACCTGGGTCCACTCCAGCGACAGACCCCTGACAAGAGCAGGTCTCTGG
 841 AGGCTGAGTTGCATGGGGCCTAGTAACACCAAGCCAGTGAGCCTCTAATGCTACTGCGCC
 901 CTGGGGGCTCCCAGGGCCTGGGCAACTTAGCTGCAACTGGCAAAGGAGAAGGGTAGTTTG
 961 AGGTGTGACACCAGTTTGCTCCAGAAAGTTTAAGGGGTCTGTTTCTCATCTCCATGGACA
1021 TCTTCAACAGCTTCACCTGACAACGACTGTTCCTATGAAGAAGCCACTTGTGTTTTAAGC
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1141 TGAGCCAAGTCAGCCTTCTGTTGGTTAATATGGTATAATGCATGGCTTTGTGCACAGCCC
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1441 TTGACCCAGTTTGTCTTTTAGGTTAAGTAAGAACTCGAGAGTAAAGGCAAGGAGGGGGGC
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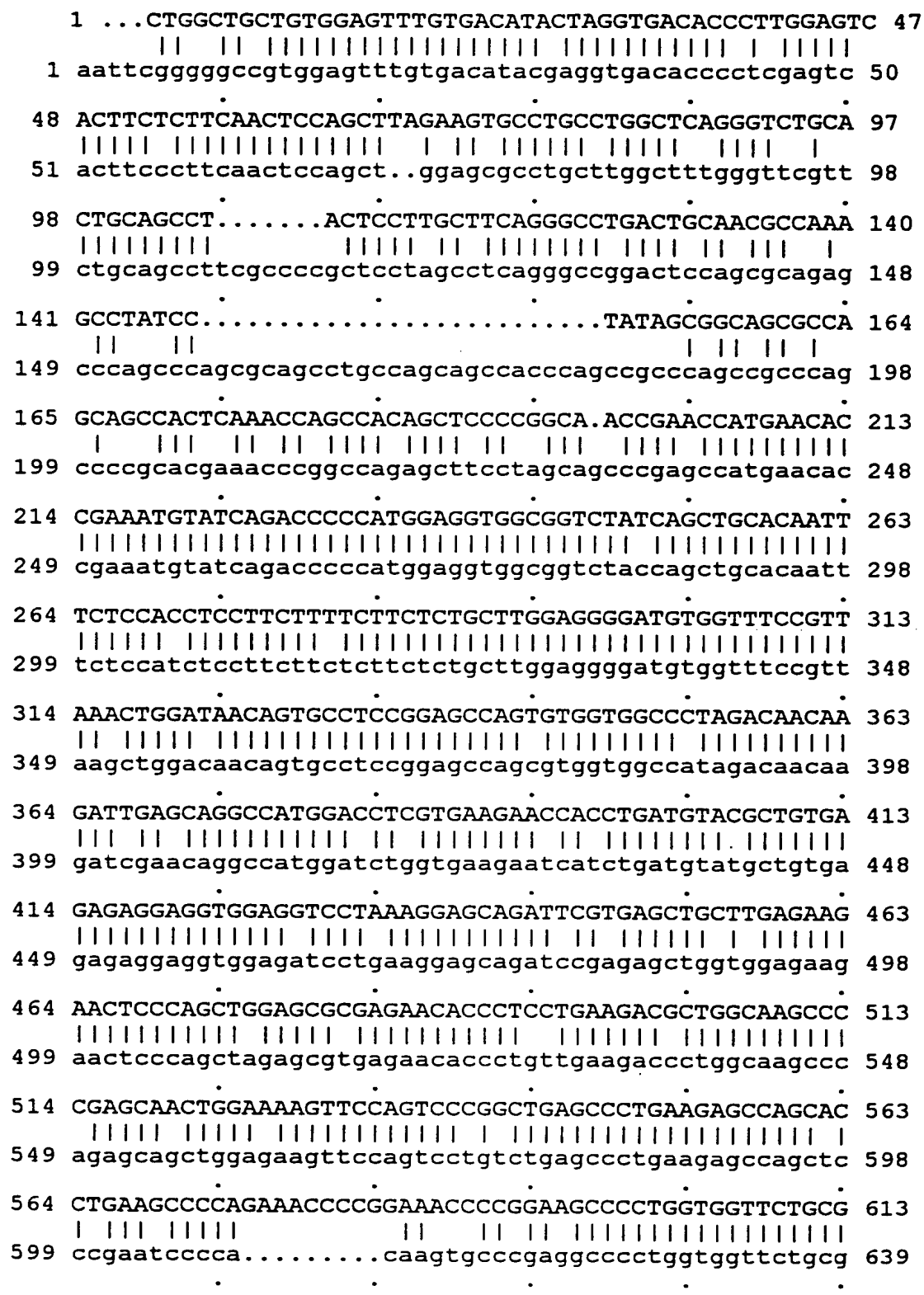
Fig. 13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51 acttcccttcaactccagct..ggagcgcctgcttggctttgggttcgtt 98
98 CTGCAGCCT.......ACTCCTTGCTTCAGGGCCTGACTGCAACGCCAAA 140
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141 GCCTATCC.....TATAGCGGCAGCGCCA 164
149 cccagcccagcgcagcctgccagcagccacccagccgcccagccgcccag 198
165 GCAGCCACTCAAACCAGCCACAGCTCCCCGGCA.ACCGAACCATGAACAC 213
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249 cgaaatgtatcagaccccatggaggtggcggtctaccagctgcacaatt 298
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299 tctccatctccttcttctcttctctgcttggaggggatgtggtttccgtt 348
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399 gatcgaacaggccatggatctggtgaagaatcatctgatgtatgctgtga 448
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449 gagaggaggtggagatcctgaaggagcagatccgagagctggtggagaag 498
464 AACTCCCAGCTGGAGCGCGAGAACACCCTCCTGAAGACGCTGGCAAGCCC 513
499 aactcccagctagagcgtgagaacaccctgttgaagaccctggcaagccc 548
514 CGAGCAACTGGAAAAGTTCCAGTCCCGGCTGAGCCCTGAAGAGCCAGCAC 563
549 agagcagctggagaagttccagtcctgtctgagccctgaagagccagctc 598
564 CTGAAGCCCCAGAAACCCCGGAAACCCCGGAAGCCCCTGGTGGTTCTGCG 613
599 ccgaatcccca.....caagtgcccgaggcccctggtggttctgcg 639

Fig. 14

```
614 GTGTAAGTGGCTCTGTCCTTAGGGTGGGCAGAGCCAC..ATCTTGTTCTA 661
    |||||||||||||||||| |||||||||||||||||  | ||||||  ||
640 gtgtaagtggctctgtcctcagggtgggcagagccactaaacttgtttta 689
    .         .         .         .         .
662 CCTAGTTCTTTCCAGTTTGTTTTTGGCTCCCCAAGGGTCATCTCATGTGG 711
    |||||||||||||||||||||||||||||||||  ||||||||  |  ||
690 cctagttctttccagtttgtttttggctccccaagcatcatctcacgagg 739
    .         .         .         .         .
712 AGAACTTTACACCTAACATAGCTGGTGCCAAGAGATGTCCCAAGGACATG 761
    ||||||||||||||| ||  ||||||||||||||||||| |||||||||
740 agaactttacacctagcacagctggtgccaagagatgtcctaaggacatg 789
    .         .         .         .         .
762 CCCATCTGGGTCCACTCCAGTGACAGACCCCTGACAAAGAGCAGGTCTCT 811
     |||  |||||||||||||| ||||||||||||| ||||||||||||||
790 gccacctgggtccactccagcgacagacccctgac.aagagcaggtctct 838
    .         .         .         .         .
812 GGAGACTAAGTTGCATGGGGCCTAGTAACACCAAGCCAGTGAGCCTGTCG 861
    ||||  ||  |||||||||||||||||||||||||||||||||||||||  |
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    .         .         .         .         .
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    ||   ||  |  |||||||||||||||||| |||||||||||| | ||  ||
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    .         .         .         .         .
911 GACCAAGGAGAAAGTAGTTTTGAGATGTGATGCCAGTGTGCTCCAGAAAG 960
    |  |  ||||||||  |    ||||||  |||||  |||||  ||||||||||||
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    .         .         .         .         .
961 TGTAAGGGGTCTGTTTTTCATTTCCATGGACATCTTCCACAGCTTCACCT 1010
    | ||||||||||||||  ||||  ||||||||||||||  ||||||||||||
989 tttaaggggtctgtttctcatctccatggacatcttcaacagcttcacct 1038
    .         .         .         .         .
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     |||||  |||||||||||||||||||||||||||||  ||||||||  ||||
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1061 CCTCTCTCTTCTTCCTCTGTCTTTTCCAGGCAGGGG.CAGAGATGGGAGA 1109
     ||||||||||| ||||||||  |   |  |||||||||  ||  ||||||||||
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1110 GATTGAGCCAAATGAGCCTTCTGTTGGTTAATACTGTATAATGCATGGCT 1159
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1160 TTGTGCACAGCCCAGTGTGGGGTTACAGCTTTGGGATGACTGCTTATAAA 1209
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     .         .         .         .         .
```

Fig. 14 (cont)

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                .         .         .         .         .
1359 GACTGGTCTCTTATCTCTTAAAGCTAAGTTTTTGACTGTGCTAATTTACC 1408
     |||||||| |||| |||||| ||||||| |||||||||| | |||||||
1388 gactggtcccttacctcttatggctaagtctttgactgtgttcatttacc 1437
                .         .         .         .         .
1409 AAATTGATCCAGTTTGTCCTTTAGATTAAATAAG.ACTCGATATGAGGGA 1457
     || |||| |||||||||| ||||| |||| |||| |||||| |  |  |
1438 aagttgacccagtttgtcttttaggttaagtaagaactcgagagtaaagg 1487
                .         .         .         .         .
1458 GGGAGGGGAAGACCAGCCTCACAATGCGGCCACAGATGCCTTGCTGCTGC 1507
         | ||  | ||||||||  |||||||||| ||||||||||||||||
1488 caaggaggggggccagcctctgaatgcggccacggatgccttgctgctgc 1537
                .         .         .         .         .
1508 AGTCC.TCCCTGATCTGTCCACTGAAGACATGAAGTCCTCTTTTGAATGC 1556
     |  || | ||  | |||||||||||| || ||||||||| ||||||||||
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                .         .         .         .         .
1557 CAAACCCACCATTCATTGGTGCTGACTACATAGAATGGGGTTGAGAGAAG 1606
     |||||||||||||| |||||||||||||||||||| ||||||||||||
1587 caaacccaccattcactggtgctgactacatagaat.gggttgagagaag 1635
                .         .         .         .         .
1607 ATCAGTTTGGACTTCACATTTTTGTTTTAAGTTTTAGGTTGTTTTTTTTT 1656
     |||||||||| ||||||| | |  ||| ||     |    |||||| |||
1636 atcagtttgggcttcacagtgtcatttgaa.....aaagcgtttttgttt 1680
                .         .         .         .         .
1657 GGTTTTGTTTGTTTGTTTGTTTGTTTGTTTTTGTTTTTTGTTTTTCTTTT 1706
      ||||||  |  ||||
1681 tgttttgaattattgt..................................  1696
                .         .         .         .         .
1707 TTAAGTTCTTGTGGGGAAACTTTGGGGTTAATCAAAGGATGTAGTCCTGT 1756
                  || |||||||   || ||   ||||||| ||||||
1697 .............ggaaaactttcaagtgaacagaaggatggtgtcctac 1733
                .         .         .         .         .
1757 GGTAGACCAG......AGGAGTAACTAGTTTTGATCCTTTGGGGTGTGGA 1800
      || ||  ||       |  ||    | | |||||||| ||| |  |||
1734 tgtggatgagggatgaacaaggggatggctttgatccaatggagcctggg 1783
                .         .         .         .         .
1801 AAATGTACCCAGGAAGCTTGTGT.AAGGAGGTTCTGTGACAGTGAACACT 1849
     |  ||| ||||| |||||||| |  ||  |||| ||||| ||||||||||
1784 aggtgtgcccagaaagcttgtctgtagcgggttttgtgagagtgaacact 1833
                .         .         .         .         .
1850 TTCCACTTTCTGACACCTCATCCTGCTGTACGACTCCAGGATTTGGATTT 1899
     ||||||||| |||||||| |||||| |||| |  ||||||||||||||||
1834 ttccacttttgacaccttatcctgatgtatggttccaggatttggattt 1883
                .         .         .         .         .
1900 GGATTTTTCAAATGTAGCTTGAAATTTCAATAAACTTTGCTCCTTTTTCT 1949
      |||||| |||||||||||||||||||||||||||||||  ||||
1884 tgattttccaaatgtagcttgaaatttcaataaactttgctctgtttttc 1933
                .         .
1950 AAAAATAAAAAAAAAAAAAAAA 1972
      |||| | |||||
1934 taaaaaataaaaa.......... 1946
```

Fig. 14 (Cont.)

```
mG     1 MNTEMYQTPMEVAVYQLHNFSTSFFSSLLGGDVVSVKLDNSASGASVVAL  50

hG     1 MNTEMYQTPMEVAVYQLHNFSISFFSSLLGGDVVSVKLDNSASGASVVAI  50
         ==================== ============================-

hT     2 KSQWCRPVAMDLGVYQLRHFSISFLSSLLGTENASVRLDNSSSGASVVAI  51
                  =---==== == == ===== - ==-====-========

mG    51 DNKIEQAMDLVKNHLMYAVREEVEVLKEQIRELLEKNSQLERENTLLKTL 100

hG    51 DNKIEQAMDLVKNHLMYAVREEVEILKEQIRELVEKNSQLERENTLLKTL 100
         ========================-========================

hT    52 DNKIEQAMDLVKSHLMYAVREEVEVLKEQIKELIEKNSQLEQENNLLKTL 101
         ============ ==================-==-=======-== =====

hD     1          MDLVKNHLMYAVREEVEILKEQIRELVEKNSQLERENTLLKTL  41
                  ================-=======-=======-========

mG   101 ASPEQLEKFQSRLSPEEPAPEAPETPETPEAPGGSAV* 138

hG   101 ASPEQLEKFQSCLSPEEPAPES...PQVPEAPGGSAV* 135
         =========== ==========-   =- =========

hT   102 ASPEQLAQFQAQLQTGSPPATTQPQGTTQPPAQPASQGSGPTA* 145
         ====== -=== =    =   -     =

hD    42 ASPEQLEKFQSCLSPEEPAPES...PQVPEAPGGSAV*
         =======-=== ==========-   ============
```

Fig. 15